Listing of the Claims

1. (Previously Presented) A method of assessing whether a subject is afflicted with prostate cancer, the method comprising comparing:

a) the level of expression of a marker in a sample from a subject, wherein the marker is selected from the group consisting of SEQ ID NO. 10 (KIAA 18) and SEQ ID NO. 11 (KIAA 96), and

b) the normal level of expression of the marker in a control sample,

wherein a significant difference between the level of expression of the marker in the sample from the subject and the normal level is an indication that the subject is afflicted with prostate cancer.

2. (Original) The method of claim 1, wherein the marker corresponds to a transcribed polynucleotide or portion thereof, wherein the polynucleotide comprises the marker.

3. (Original) The method of claim 1, wherein the sample comprises cells obtained from the subject.

4. (Original) The method of claim 3, wherein the cells are collected from the prostate gland.

5. (Original) The method of claim 3, wherein the cells are collected from blood.

6. (Original) The method of claim 1, wherein the level of expression of the marker in the sample differs from the normal level of expression of the marker in a subject not afflicted with prostate cancer by a factor of at least about 2.

7. (Original) The method of claim 1, wherein the level of expression of the marker in the sample differs from the normal level of expression of the marker in a subject not afflicted with prostate cancer by a factor of at least about 3.

8. (Original) The method of claim 1, wherein the marker is not significantly expressed in non-prostate cancer cells.

9. (Original) The method of claim 1, wherein the level of expression of the marker in the sample is assessed by detecting the presence in the sample of a protein corresponding to the marker.

10. (Original) The method of claim 9, wherein the presence of the protein is detected using a reagent which specifically binds with the protein.

11. (Original) The method of claim 10, wherein the reagent is selected from the group consisting of an antibody, an antibody derivative, and an antibody fragment.

12. (Original) The method of claim 1, wherein the level of expression of the marker in the sample is assessed by detecting the presence in the sample of a transcribed polynucleotide or portion thereof, wherein the transcribed polynucleotide comprises the marker.

13. (Original) The method of claim 12, wherein the transcribed polynucleotide is an mRNA.

14. (Original) The method of claim 12, wherein the transcribed polynucleotide is a cDNA.

15. (Original) The method of claim 12, wherein the step of detecting further comprises amplifying the transcribed polynucleotide.

16. (Original) The method of claim 1, wherein the level of expression of the marker in the sample is assessed by detecting the presence in the sample of a transcribed polynucleotide which anneals with the marker or anneals with a portion of a polynucleotide, wherein the polynucleotide comprises the marker, under stringent hybridization conditions.

17. (Previously Presented) The method of claim 1, further comprising comparing:

a) the level of expression in the sample of each of at least two markers independently, wherein the markers are selected from the group consisting of SEQ ID NO. 10 (KIAA 18) and SEQ ID NO. 11 (KIAA 96); and

b) the normal level of expression of the at least two markers in samples of the same type obtained from control subjects not afflicted prostate cancer,
wherein the level of expression of more than one of the markers is significantly altered, relative to the corresponding normal levels of expression of the markers, is an indication that the subject is afflicted prostate cancer.

18. (Previously Presented) A method for monitoring the progression of prostate cancer in a subject, the method comprising:

a) detecting in a subject sample at a first point in time, the expression of a marker, wherein the marker is selected from the group consisting of the markers SEQ ID NO. 10 (KIAA 18) and SEQ ID NO. 11 (KIAA 96) or a combination thereof;

b) repeating step a) at a subsequent point in time; and

c) comparing the level of expression detected in steps a) and b), and therefrom monitoring the progression of prostate cancer in the subject.

19. (Original) The method of claim 18, wherein marker corresponds to a transcribed polynucleotide or portion thereof, wherein the polynucleotide comprises the marker.

20. (Original) The method of claim 18, wherein the sample comprises cells obtained from the subject.

21. (Original) The method of claim 20, wherein the cells are collected from the prostate gland.

22. (Original) The method of claim 20, wherein the cells are collected from blood.

23. – 50. (Canceled)

51. (Previously Presented) The method of claim 1, wherein the marker is SEQ ID NO. 10 (KIAA 18).

52. (Previously Presented) The method of claim 1, wherein the marker is SEQ ID NO. 11 (KIAA 96).

53. (Previously Presented) The method of claim 18, wherein the marker is SEQ ID NO. 10 (KIAA 18).

54. (Previously Presented) The method of claim 18, wherein the marker is SEQ ID NO. 11 (KIAA 96).